P77

Functional Analysis of Fur in Virulence of *Pseudomonas syringae* pv. tabaci 11528: Fur Controls Expression of Genes Involved in Quorum-Sensing Regulation

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In most bacteria, Fur (ferric uptake regulator) is a crucial global regulator, which is known to operate not only in the regulation of iron homeostasis, but also in a variety of other cellular processes. In an effort to characterize the role of Fur in the virulence of plant pathogens, we isolated a *fur* homologue from *Pseudomonas syringae* pv. *tabaci* 11528, which showed significant sequence homology to the *fur* genes in other *P. syringae* pathovars. In phenotype assays of a *fur* deletion mutant (BL33) constructed via marker exchange mutagenesis using a suicide vector, we observed that BL33 grows slowly and reaches stationary phase at a lower cell density than does its parental strain, and constitutively produced siderophore(s) in CAS plate assays. Unlike effect on siderophore(s) synthesis of a *fur* mutation, motility and tabtoxin production were repressed in BL33, thereby suggesting that Fur may coregulate swarming motility and tabtoxin production with other regulators. Interestingly, the results of TLC indicated that Fur positively controlled the synthesis of quorum-sensing (QS) autoinducers (*N*-acyl homoserine lactones). Thus, we further conducted an inspection of the consensus Fur-box in the putative promoter regions and quantitative real-time RT-PCR of QS-associated genes, *psyR* and *psyI*. Consistent with the results of TLC, putative Fur-box regions were identified in their putative promoter regions, and Fur was shown to upregulate the genes at the transcriptional level. Finally, the effects of a *fur* mutation on plant virulence indicated that Fur-regulated traits may be relevant with regard to the plant-pathogen interaction.

Key word: Pseudomonas syringae pv. tabaci 11528, Fur(ferric uptake regulator), QS(quorum-sensing), quantitative real-time RT-PCR

P78

Members of the bHLH-PAS Family Regulate *Drosophila mmp2* Transcription in *Drosophila* Visual System

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Matirx metalloproteinases (MMPs) are a family of proteolytic enzyme that promote turnover of almost components of the extracellular matrix (ECM). In the central nervous system (CNS), MMPs have been shown to degrade components of the basal lamina, leading to disruption of the blood-brain barrier (BBB), and to contribute to the neuro-inflammatory response in many neurological diseases. Brain cells express some kinds of MMPs and TIMP in response to cellular stress. Of the two *Drosophila* MMPs, only *mmp2* is expressed in the CNS. We show here that the expression of *Drosophila mmp2*, which directs reporter expression to portions of the larval lamina, overlaps with the expression of *Drosophila single-minded* (*sim*) which encodes a basic helix-loop-helix PAS (bHLH-PAS) domain containing transcriptional regulator. We found that there is a SIM::TGO heterodimer binding site (CME; central midline element) in the promoter region of *Drosophila mmp2*. Upon site-directed mutagenesis, we found that the CME site on the promoter region of *mmp2* was required for the promoter activity of *mmp2* gene. In addition, we found that SIM overexpressed fly has abnormal photoreceptor phenotype in larval and adult brain, which was rescued by inhibition of MMP2 using UAS-mmp2 RNAi. Taken together, our results suggest that the member of bHLH-PAS family, SIM, regulate *Drosophila mmp2* transcription in visual system of *Drosophila*.

Key words: Drosophila, MMP, SIM